

EXHIBIT 4

DR EMBL; AE004969; AAW90230.1; -; Genomic_DNA.
DR RefSeq; YP_208642.1; -.
DR HSSP; P15770; 1NYT.
DR STRING; Q5F6F7; -.
DR GeneID; 3281609; -.
DR GenomeReviews; AE004969_GR; NGO1602.
DR KEGG; ngo:NGO1602; -.
DR NMPDR; fig|242231.4.peg.1691; -.
DR HOGENOM; HBG553408; -.
DR OMA; DLYCVMG; -.
DR BioCyc; NGON242231:NGO1602-MON; -.
DR GO; GO:0005737; C:cytoplasm; IEA:InterPro.
DR GO; GO:0050661; F:NADP or NADPH binding; IEA:InterPro.
DR GO; GO:0004764; F:shikimate 5-dehydrogenase activity; IEA:HAMAP.
DR GO; GO:0009073; P:aromatic amino acid family biosynthetic pro...;
IEA:HAMAP.
DR GO; GO:0055114; P:oxidation reduction; IEA:UniProtKB-KW.
DR HAMAP; MF_00222; -; 1.
DR InterPro; IPR016040; NAD(P)-bd_dom.
DR InterPro; IPR011342; Quinate/shikimate_5-DH.
DR InterPro; IPR013708; Shikimate_DH-bd_N.
DR InterPro; IPR006151; Shikm_DH/Glu-tRNA_Rdtase.
DR Gene3D; G3DSA:3.40.50.720; NAD(P)-bd; 1.
DR Pfam; PF01488; Shikimate_DH; 1.
DR Pfam; PF08501; Shikimate_dh_N; 1.
PE 3: Inferred from homology;
KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
KW Complete proteome; NADP; Oxidoreductase.
FT CHAIN 1 269 Shikimate dehydrogenase.
FT /FTId=PRO_1000021311.
FT NP_BIND 130 134 NADP (By similarity).
FT ACT_SITE 68 68 Proton acceptor (Potential).
SQ SEQUENCE 269 AA; 28649 MW; 07FFD1FCF1A5FDD9 CRC64;
MHALPRYAVF GNPAHASKSP QIHQQFALQE GVDIEYGRIC ADIGGFAQAV STFFETGGCG
ANVTVPFKQE AFHLADEHSD RALAAGAVNT LVWLEDGRIR GDNTDGIGLA NDITQVKNIA
IEGKTILLLG AGGAVRGVIP VLKEHRPARI VIANRTRAKA EELARLFGIE AVPMADVNGG
FDIIINGTSG GLSGQLPAVS PKIFRDCRLA YDMVYGAAK PFLDFARQSG AKKTADGLGM
LVGQAAASYA LWRGFKPDIR PVIEHMKAL

DR EMBL; AE004969; AAW90292.1; -; Genomic_DNA.
DR RefSeq; YP_208704.1; -.
DR STRING; Q5F695; -.
DR GeneID; 3281268; -.
DR GenomeReviews; AE004969_GR; NGO1667.
DR KEGG; ngo:NGO1667; -.
DR NMPDR; fig|242231.4.peg.1808; -.
DR HOGENOM; HBG704071; -.
DR OMA; MVDTWVT; -.
DR BioCyc; NGON242231:NGO1667-MON; -.
DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
DR GO; GO:0008666; F:2,3,4,5-tetrahydropyridine-2,6-dicarboxylat...;
IEA:HAMAP.

DR GO; GO:0019877; P:diaminopimelate biosynthetic process; IEA:HAMAP.
 DR HAMAP; MF_00811; -; 1.
 DR InterPro; IPR005664; DapD.
 DR InterPro; IPR001451; Hexapep_transf.
 DR InterPro; IPR018357; Hexapep_transf_CS.
 DR InterPro; IPR011004; Trimer_LpxA-like.
 DR Pfam; PF00132; Hexapep; 4.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
 PE 3: Inferred from homology;
 KW Acyltransferase; Amino-acid biosynthesis; Complete proteome;
 KW Cytoplasm; Diaminopimelate biosynthesis; Lysine biosynthesis;
 Repeat;
 KW Transferase.
 FT CHAIN 1 273 2,3,4,5-tetrahydropyridine-2,6-
 FT dicarboxylate N-succinyltransferase.
 FT /FTId=PRO_0000196950.
 FT BINDING 104 104 Substrate (By similarity).
 FT BINDING 141 141 Substrate (By similarity).
 SQ SEQUENCE 273 AA; 29305 MW; 762DD5A632781146 CRC64;
 MSLQNIETA FENRADITPT TVAPEVKEAV LETIRQLDSG KLRVAERLGV GEWKVNEWAK
 KAVLLSFRIQ DNEVLNDGVN KYFDKVPTKF ADWSEDEFKN AGFRAVPGAV ARRGSFVAKN
 AVLMPYSYVNI GAYVDEGAMV DTWATVGSCA QIGKNVHLSG GVGIGGVLEP LQAAPTIIED
 NCFIGARSEI VEGAIVEEGS VISMGVFIGQ STKIFDRTTG EIYQGRVPAG SVVVSGLPS
 KDGSHSLYCA VIVKRVDAT RAKTSVNELL RGI

 DR EMBL; AE004969; AAW89131.1; -; Genomic_DNA.
 DR RefSeq; YP_207543.1; -.
 DR PDB; 3D1T; X-ray; 2.20 A; A/B=1-257.
 DR PDB; 3D2O; X-ray; 2.04 A; A/B=1-257.
 DR PDBsum; 3D1T; -.
 DR PDBsum; 3D2O; -.
 DR STRING; Q5F9K6; -.
 DR GeneID; 3282560; -.
 DR GenomeReviews; AE004969_GR; NGO0387.
 DR KEGG; ngo:NGO0387; -.
 DR NMPDR; fig|242231.4.peg.732; -.
 DR HOGENOM; HBG626871; -.
 DR OMA; SLMDYEV; -.
 DR BioCyc; NGON242231:NGO0387-MON; -.
 DR GO; GO:0003934; F:GTP cyclohydrolase I activity; IEA:EC.
 DR HAMAP; MF_01527; -; 1.
 DR InterPro; IPR003801; DUF198.
 DR Pfam; PF02649; DUF198; 1.
 PE 1: Evidence at protein level;
 KW 3D-structure; Complete proteome; Hydrolase.
 FT CHAIN 1 257 GTP cyclohydrolase folE2.
 FT /FTId=PRO_0000147714.
 FT SITE 147 147 May be catalytically important (By
 FT similarity).
 FT STRAND 18 21
 FT STRAND 26 32
 FT STRAND 39 47
 FT STRAND 49 51
 FT HELIX 61 69
 FT HELIX 76 89
 FT STRAND 97 108

FT STRAND 115 125
 FT STRAND 136 146
 FT HELIX 148 153
 FT STRAND 160 173
 FT HELIX 178 185
 FT STRAND 188 191
 FT HELIX 198 210
 FT HELIX 215 228
 FT STRAND 232 241
 FT STRAND 246 256
 SQ SEQUENCE 257 AA; 28747 MW; A0235399C3EDF2A9 CRC64;
 MNAIADVQSS RDLRNLPINQ VGIKDLRFPI TLKTAEGTQS TVARLTMTVY LPAEQKGTHM
 SRFVALMEQH TEVLDFQALH RLTAEMVALL DSRAGKISVS FPFFRKKTAP VSGIRSLLDY
 DVSLTGEMKD GAYGHSMKVM IPVTSLCPCS KEISQYGAHN QRSHVTVSLT SDAEVGIEEV
 IDYVETQASC QLYGLLKRPD EKYVTEKAYE NPKFVEDMVR DVATSLIADK RIKSFVVESE
 NFESIHNHSA YAYIAYP

DR EMBL; AE004969; AAW90424.1; -; Genomic_DNA.
 DR RefSeq; YP_208836.1; -.
 DR HSSP; P0A722; 1LXA.
 DR STRING; Q5F5W3; -.
 DR GeneID; 3282363; -.
 DR GenomeReviews; AE004969_GR; NGO1806.
 DR KEGG; ngo:NGO1806; -.
 DR NMPDR; fig|242231.4.peg.1389; -.
 DR HOGENOM; HBG659295; -.
 DR OMA; GHTSIGE; -.
 DR BioCyc; NGON242231:NGO1806-MON; -.
 DR GO; GO:0005737; C:cytoplasm; IEA:UniProtKB-SubCell.
 DR GO; GO:0008780; F:acyl-[acyl-carrier-protein]-UDP-N-acetylglu...;
 IEA:HAMAP.
 DR GO; GO:0009245; P:lipid A biosynthetic process; IEA:HAMAP.
 DR HAMAP; MF_00387; -; 1.
 DR InterPro; IPR001451; Hexapep_transf.
 DR InterPro; IPR010137; Lipid_A_lpxA.
 DR InterPro; IPR011004; Trimer_LpxA-like.
 DR Pfam; PF00132; Hexapep; 6.
 DR PIRSF; PIRSF000456; UDP-GlcNAc_acltr; 1.
 DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
 PE 3: Inferred from homology;
 KW Acyltransferase; Complete proteome; Cytoplasm; Lipid A
 biosynthesis;

KW Lipid synthesis; Repeat; Transferase.
 FT CHAIN 1 258 Acyl-[acyl-carrier-protein]--UDP-N-
 FT acetylglucosamine O-acyltransferase.
 FT /FTId=PRO_0000302582.
 SQ SEQUENCE 258 AA; 28171 MW; B8B5D9D2EE8CCDD3 CRC64;
 MTLIHPTAVI DPKAELDSGV KVGAYTVIGP NVRIGANTEI GPHAVINGHT TIGENNRIFQ
 FASLGEIPQD KKYRDEPTKL IIGNGNTIRE FTTFNLGTVT GIGETRIGDD NWIMAYCHLA
 HDCVVGNHIT FANNASLAGH VTVGDYVVLG GYTLVFQFCR IGDYAMTAFA AGVHKDVPPY
 FMASGYRAEP AGLNSEGMRR NGFTAQISA VKDVYKTLYH RGIPFEEAKA DILRRAETQA
 ELAVFQDFFA QSTRGIIR

DR EMBL; AE004969; AAW90138.1; -; Genomic_DNA.
 DR RefSeq; YP_208550.1; -.

DR HSSP; P94556; 1ZUW.
 DR STRING; Q5F6P9; -.
 DR GeneID; 3281584; -.
 DR GenomeReviews; AE004969_GR; NGO1500.
 DR KEGG; ngo:NGO1500; -.
 DR NMPDR; fig|242231.4.peg.1517; -.
 DR HOGENOM; HBG645102; -.
 DR OMA; NSPPREV; -.
 DR BioCyc; NGON242231:NGO1500-MON; -.
 DR GO; GO:0008881; F:glutamate racemase activity; IEA:HAMAP.
 DR GO; GO:0007047; P:cell wall organization; IEA:UniProtKB-KW.
 DR GO; GO:0009252; P:peptidoglycan biosynthetic process; IEA:HAMAP.
 DR GO; GO:0008360; P:regulation of cell shape; IEA:UniProtKB-KW.
 DR HAMAP; MF_00258; -; 1.
 DR InterPro; IPR015942; Asp/Glu/hydantoin_racemase.
 DR InterPro; IPR001920; Asp/Glu_race.
 DR InterPro; IPR018187; Asp/Glu_racemase_AS.
 DR InterPro; IPR004391; Glu_race.
 DR Gene3D; G3DSA:3.40.50.1860; Asp/Glu_race; 1.
 DR Pfam; PF01177; Asp_Glu_race; 1.
 DR PROSITE; PS00923; ASP_GLU_RACEMASE_1; FALSE_NEG.
 DR PROSITE; PS00924; ASP_GLU_RACEMASE_2; 1.
 PE 3: Inferred from homology;
 KW Cell shape; Cell wall biogenesis/degradation; Complete proteome;
 KW Isomerase; Peptidoglycan synthesis.
 FT CHAIN 1 270 Glutamate racemase.
 FT /FTid=PRO_1000047589.
 SQ SEQUENCE 270 AA; 29515 MW; 913E8ABBA2805564 CRC64;
 MENIGRQRPI GVFD SGIGGL TNVRALMERL PMENIIYFGD TARVPYGTKS KATIENFSMQ
 IVDFLLGHDV KAMVIACNTI AAVAGRKIRQ KTGNNMPVLDV ISAGAKAALA TTRNNKIGII
 ATNTTVNSNA YARAIHRDNP DTLVRTQAAP LLVPLVEEGW LEHEVTRLTV CEYLKPLLAD
 GIDTLVLGCT HFPLLKPLIG REAHNVALVD SAITTAETA RVLAQEGLLD TGNNNPDYRF
 YVSDIPLKFR TIGERFLGRT MEQIEMVSLG

DR EMBL; AE004969; AAW89865.1; -; Genomic_DNA.
 DR RefSeq; YP_208277.1; -.
 DR STRING; Q5F7H2; -.
 DR GeneID; 3281969; -.
 DR GenomeReviews; AE004969_GR; NGO1206.
 DR KEGG; ngo:NGO1206; -.
 DR NMPDR; fig|242231.4.peg.1064; -.
 DR HOGENOM; HBG541103; -.
 DR OMA; IFMSVFN; -.
 DR BioCyc; NGON242231:NGO1206-MON; -.
 DR GO; GO:0048037; F:cofactor binding; IEA:InterPro.
 DR GO; GO:0004609; F:phosphatidylserine decarboxylase activity;
 IEA:HAMAP.
 DR GO; GO:0006646; P:phosphatidylethanolamine biosynthetic process;
 IEA:InterPro.
 DR HAMAP; MF_00664; -; 1.
 DR InterPro; IPR003817; PS_Dcarbxyase.
 DR InterPro; IPR004428; PtdSer_deCO2ase_related.
 DR Pfam; PF02666; PS_Dcarbxyase; 1.
 PE 3: Inferred from homology;

KW Complete proteome; Decarboxylase; Lyase; Phospholipid biosynthesis;

KW Pyruvate; Zymogen.

FT CHAIN 1 182 Phosphatidylserine decarboxylase beta chain (By similarity).
 FT /FTId=PRO_0000042279.
 FT CHAIN 183 259 Phosphatidylserine decarboxylase alpha chain (By similarity).
 FT /FTId=PRO_0000042280.
 FT SITE 182 183 Cleavage (non-hydrolytic) (By similarity).
 FT MOD_RES 183 183 Pyruvic acid (Ser) (By similarity).

SQ SEQUENCE 259 AA; 28294 MW; A4D013CF6066A7BE CRC64;
 MNRLYPHPPII AREGWPIIGG GLALSLLVSM CCGWWSLPFW VFTVFALQFF RDPAREIPQN
 PEAVLSPVDG RIVVVERARD PYRDVDALKI SIFMNVFNVH SQKSPADCTV TKVVYNKGKF
 VNADLDKAST ENERNAVLAT TASGREITFV QVAGLVARRI LCYTQAGAKL SRGERYGFI
 FGSRVDMYLP VDAQAQVAIG DKVTGVKTVL ARLPLTDSQA DPVSQAASVE TAANPSAEQQ
 QIEAAAAKIQ AAVQDVLKD

DR EMBL; AE004969; AAW90342.1; -; Genomic_DNA.
 DR RefSeq; YP_208754.1; -.
 DR HSSP; P00909; 1PII.
 DR STRING; Q5F645; -.
 DR GeneID; 3281235; -.
 DR GenomeReviews; AE004969_GR; NGO1721.
 DR KEGG; ngo:NGO1721; -.
 DR NMPDR; fig|242231.4.peg.1924; -.
 DR HOGENOM; HBG540956; -.
 DR OMA; PLLCKDF; -.
 DR BioCyc; NGON242231:NGO1721-MON; -.
 DR GO; GO:0004425; F:indole-3-glycerol-phosphate synthase activity; IEA:HAMAP.
 DR GO; GO:0000162; P:tryptophan biosynthetic process; IEA:HAMAP.
 DR HAMAP; MF_00134; -; 1.
 DR InterPro; IPR013785; Aldolase_TIM.
 DR InterPro; IPR013798; Indole-3-glycerol_P_synth.
 DR InterPro; IPR001468; Indole-3-GPS_central.
 DR InterPro; IPR011060; RibuloseP-bd_barrel.
 DR Gene3D; G3DSA:3.20.20.70; Aldolase_TIM; 1.
 DR Pfam; PF00218; IGPS; 1.
 DR PROSITE; PS00614; IGPS; 1.
 PE 3: Inferred from homology;
 KW Amino-acid biosynthesis; Aromatic amino acid biosynthesis;
 KW Complete proteome; Decarboxylase; Lyase; Tryptophan biosynthesis.

FT CHAIN 1 260 Indole-3-glycerol phosphate synthase.
 FT /FTId=PRO_1000018508.

SQ SEQUENCE 260 AA; 28622 MW; 097107AE32AD93AB CRC64;
 MTDILNKILA TKAQEVAQK AAVNAEHIRA LAEEAAPVRS FIDSIRGKHR LNLPAVIAEI
 KKASPSKGLI RPDFRPAEIA RAYENAGAAC LSVLTDEPYF QGSPEYLKQA REAVLLPVLR
 KDFIIDEYQV YQARAWGADA VLLIAAALEQ GQLERFEALA HELGMTVLLE LHDETELEKC
 RNLTTPLWGV NNRNLRTFEV SLDQTLSELLP ALEGKTVVTE SGITGKADVE FMRARGVHTF
 LIGETFMRAD DIGAEVGKLF

DR EMBL; AE004969; AAW90429.1; -; Genomic_DNA.
 DR RefSeq; YP_208841.1; -.
 DR STRING; Q5F5V8; -.
 DR GeneID; 3282256; -.
 DR GenomeReviews; AE004969_GR; NGO1811.
 DR KEGG; ngo:NGO1811; -.
 DR NMPDR; fig|242231.4.peg.1394; -.
 DR HOGENOM; HBG621020; -.
 DR OMA; QSKTPFR; -.
 DR BioCyc; NGON242231:NGO1811-MON; -.
 DR GO; GO:0009982; F:pseudouridine synthase activity; IEA:HAMAP.
 DR GO; GO:0003723; F:RNA binding; IEA:InterPro.
 DR GO; GO:0031119; P:tRNA pseudouridine synthesis; IEA:HAMAP.
 DR HAMAP; MF_00171; -; 1.
 DR InterPro; IPR020103; PsdUridine_synth_cat_dom.
 DR InterPro; IPR001406; PsdUridine_synth_TrueA.
 DR InterPro; IPR020097; PsdUridine_synth_TrueA_a/b_dom.
 DR InterPro; IPR020095; PsdUridine_synth_TrueA_C.
 DR InterPro; IPR020094; PsdUridine_synth_TrueA_N.
 DR Gene3D; G3DSA:3.30.70.580; PseudoU_synth_1; 1.
 DR Gene3D; G3DSA:3.30.70.660; PseudoU_synth_1; 1.
 DR PANTHER; PTHR11142; PseudoU_synth_1; 1.
 DR Pfam; PF01416; PseudoU_synth_1; 2.
 DR PIRSF; PIRSF001430; tRNA_psdUrid_synth; 1.
 PE 3: Inferred from homology;
 KW Complete proteome; Isomerase; tRNA processing.
 FT CHAIN 1 265 tRNA pseudouridine synthase A.
 FT /FTId=PRO_0000057418.
 FT ACT_SITE 58 58 Nucleophile (By similarity).
 SQ SEQUENCE 265 AA; 28806 MW; 4A69B5CE60B97A48 CRC64;
 MDTAQKQKQWA ITLSYDGSRF YGWQKQAGGV PTVQAALETA LARIAGESVA TTVAGRTDTG
 VHATAQVVHF DTA AVRPAQA WIRGVNAHLP EGI AVLHARQ VAPGFHARFD ASGRHYRYLL
 ESAPVRSPLL KNRAGWTHLE LDIGPMRRAA ALLVGEQDFS SFRAAGCQAK SPVKTIYRAD
 LTQSAGLVRL DLHGNAFLHH MVRNIMGALV YVSGRSLVE GFAALI QERS RLKAPPTFMP
 DGLYLTGV DY PGAYGIVRPQ IPEWL

DR EMBL; AE004969; AAW89536.1; -; Genomic_DNA.
 DR RefSeq; YP_207948.1; -.
 DR STRING; Q5F8F1; -.
 DR GeneID; 3282206; -.
 DR GenomeReviews; AE004969_GR; NGO0826.
 DR KEGG; ngo:NGO0826; -.
 DR NMPDR; fig|242231.4.peg.120; -.
 DR HOGENOM; Q5F8F1; -.
 DR OMA; MWIDDIY; -.
 DR PhylomeDB; Q5F8F1; -.
 DR BioCyc; NGON242231:NGO0826-MON; -.
 DR InterPro; IPR002110; Ankyrin_rpt.
 DR InterPro; IPR020683; Ankyrin_rpt-contain_dom.
 DR InterPro; IPR018756; DUF2314.
 DR Gene3D; G3DSA:1.25.40.20; ANK; 1.
 DR Pfam; PF00023; Ank; 1.
 DR Pfam; PF10077; DUF2314; 1.
 DR SMART; SM00248; ANK; 1.
 DR PROSITE; PS50297; ANK_REP_REGION; 1.

DR PROSITE; PS50088; ANK_REPEAT; 1.
PE 4: Predicted;
KW Complete proteome.
SQ SEQUENCE 252 AA; 28937 MW; 5F1A9BEDFADD1740 CRC64;
MGDSVIYYVE QADEPVNRAG ERARKTFKYF WRELFWERRR IISALDFAMV KVPFFQDGED
GEICEHMMWID DIYFDGLYIY GVLNNEPGGL TNVEQGESVC VPVGDISDWM FVCNGIPYGG
FTVQAMRGQM TEEERTEHDT AWGIDFGDPG QVLPVYEEKE HPENLEEHPM CRNCIDDFRQ
QLSQNPDFLH EQDEDGYTPL HHEAMAGNAL MVQAMLEYGA NPASKTSEGY TALDFARLTG
WQNVADLLEP RH